FIG. 1A

```
1    ACCTGAGTAA GAGCTTGGAA AAGTTGAGCC CTCTTCGAGA GAAATTGGAA GAACAGTTTA AGAGGCTGCT ATTCCAAAAA GCTTTCAACT CTCAGCAGTT
     TGGACTCATT CTCGAACCTT TTCAACTCGG GAGAAGCTCT CTTTAACCTT CTTGTCAAAT TCTCCGACGA TAAGGTTTTT CGAAAGTTGA GAGTCGTCAA

101  AGTTCATGTC ATTGTCATTA ACCTGTTTCA ACTTCATCAC CTTCGTGACT TTAGCAATGA AACCGAGCAG CACACTTATA GCCAAGATGA GCAGCTATGT
     TCAAGTACAG TAACAGTAAT TGGACAAAGT TGAAGTAGTG GAAGCACTGA AATCGTTACT TTGGCTCGTC GTGTGAATAT CGGTTCTACT CGTCGATACA

+3                          MetSer PheLeuGlyIle LeuCysLys CysProLeu GlnAsnGluSer GlnGluGlu SerTyrAsn AlaTyrProLeu
                            ----------------------------------------------------------------------------------
201  TGGACACAGT TGCTGGCCCT CTTTATGTCT TTTCTTGGCA TCCTGTGCAA GTGTCCTCTA CAGAATGAGT CTCAGGAGGA GTCCTACAAT GCCTATCCTC
     ACCTGTGTCA ACGACCGGGA GAAATACAGA AAAGAACCGT AGGACACGTT CACAGGAGAT GTCTTACTCA GAGTCCTCCT CAGGATGTTA CGGATAGGAG

+3   LeuProAlaVal LysValSer MetAspTrpLeu ArgLeuArg ProArgVal PheGlnGluAla ValValAsp GluArgGln TyrIleTrpPro TrpLeuIle
     ----------------------------------------------------------------------------------------------------------
301  TTCCAGCAGT CAAGGTCTCC ATGGACTGGC TAAGACTCAG ACCCAGGGTC TTTCAGGAGG CAGTGGTGGA TGAAAGACAG TACATTTGGC CCTGGTTGAT
     AAGGTCGTCA GTTCCAGAGG TACCTGACCG ATTCTGAGTC TGGGTCCCAG AAAGTCCTCC GTCACCACCT ACTTTCTGTC ATGTAAACCG GGACCAACTA

+3 IleSerLeuLeu AsnSerPheHis ProHisGlu GluAspLeu SerSerIleSer AlaThrPro LeuProGlu GluPheGluLeu GlnGlyPhe LeuAlaLeu
   ----------------------------------------------------------------------------------------------------------
401  TTCTCTTCTG AATAGTTTCC ATCCCCATGA AGAGGACCTC TCAAGTATTA GTGCGACACC ACTTCCAGAG GAGTTTGAAT TACAAGGATT TTTGGCATTG
     AAGAGAAGAC TTATCAAAGG TAGGGGTACT TCTCCTGGAG AGTTCATAAT CACGCTGTGG TGAAGGTCTC CTCAAACTTA ATGTTCCTAA AAACCGTAAC

+3   ArgProSerPhe ArgAsnLeu AspPheSer LysGlyHisGln GlyIleThr GlyAspLys GluGlyGlnGln ArgArgIle ArgGlnGln ArgLeuIleSer
     ----------------------------------------------------------------------------------------------------------
501  AGACCTTCTT TCAGGAACTT GGATTTTTCC AAAGGTCACC AGGGTATTAC AGGGGACAAA GAAGGCCAGC AACGACGAAT ACGACAGCAA CGCTTGATCT
     TCTGGAAGAA AGTCCTTGAA CCTAAAAAGG TTTCCAGTGG TCCCATAATG TCCCCTGTTT CTTCCGGTCG TTGCTGCTTA TGCTGTCGTT GCGAACTAGA

+3   SerIleGlyLys TrpIleAla AspAsnGlnPro ArgLeuIle GlnCysGlu AsnGluValGly LysLeuLeu PheIleThr GluIleProGlu LeuIleLeu
     ----------------------------------------------------------------------------------------------------------
601  CTATAGGCAA ATGGATTGCT GATAATCAGC CAAGGCTGAT TCAGTGTGAA AATGAGGTAG GGAAATTGTT GTTTATCACA GAAATCCCAG AATTAATACT
     GATATCCGTT TACCTAACGA CTATTAGTCG GTTCCGACTA AGTCACACTT TTACTCCATC CCTTTAACAA CAAATAGTGT CTTTAGGGTC TTAATTATGA

+3 LeuGluAspPro SerGluAlaLys GluAsnLeu IleLeuGln GluThrSerVal IleGluSer LeuAlaAla AspGlySerPro GlyLeuLys SerValLeu
   ----------------------------------------------------------------------------------------------------------
701  GGAAGACCCC AGTGAAGCCA AAGAGAACCT CATTCTGCAA GAAACATCTG TGATAGAGTC GCTGGCTGCA GATGGGAGCC CAGGGCTAAA ATCAGTGCTA
     CCTTCTGGGG TCACTTCGGT TTCTCTTGGA GTAAGACGTT CTTTGTAGAC ACTATCTCAG CGACCGACGT CTACCCTCGG GTCCCGATTT TAGTCACGAT
```

FIG. 1B

```
+3   SerThrSerArg AsnLeuSer AsnAsnCys AspThrGlyGlu LysProVal ValThrPhe LysGluAsnIle LysThrArg GluValAsn ArgAspGlnGly
     ----------------------------------------------------------------------------------------------------
801  TCTACAAGCC GAAATTTAAG CAACAACTGT GACACAGGAG AGAAGCCAGT GGTTACCTTC AAAGAAAACA TTAAGACACG AGAAGTGAAC AGAGACCAAG
     AGATGTTCGG CTTTAAATTC GTTGTTGACA CTGTGTCCTC TCTTCGGTCA CCAATGGAAG TTTCTTTTGT AATTCTGTGC TCTTCACTTG TCTCTGGTTC

+3   GlyArgSerPhe ProProLys GluValArgArg AspTyrSer LysGlyIle ThrValThrLys AsnAspGly LysLysAsp AsnAsnLysArg LysThrGlu
     ----------------------------------------------------------------------------------------------------
901  GAAGAAGTTT TCCTCCCAAA GAGGTGAGAA GGGACTATAG CAAAGGAATA ACTGTAACTA AGAATGATGG AAAGAAGGAC AACAACAAGA GGAAAACTGA
     CTTCTTCAAA AGGAGGGTTT CTCCACTCTT CCCTGATATC GTTTCCTTAT TGACATTGAT TCTTACTACC TTTCTTCCTG TTGTTGTTCT CCTTTTGACT

+3   GluThrLysLys CysThrLeuGlu LysLeuGln GluThrGly LysGlnAsnVal AlaValGln ValLysSer GlnThrGluLeu ArgLysThr ProValSer
     ----------------------------------------------------------------------------------------------------
1001 AACCAAGAAA TGCACCTTAG AAAAGTTACA GGAAACAGGA AAGCAGAATG TGGCAGTGCA GGTAAAATCC CAGACAGAAC TAAGAAAGAC TCCAGTGTCT
     TTGGTTCTTT ACGTGGAATC TTTTCAATGT CCTTTGTCCT TTCGTCTTAC ACCGTCACGT CCATTTTAGG GTCTGTCTTG ATTCTTTCTG AGGTCACAGA

+3   GluAlaArgLys ThrProVal ThrGlnThr ProThrGlnAla SerAsnSer GlnPheIle ProIleHisHis ProGlyAla PheProPro LeuProSerArg
     ----------------------------------------------------------------------------------------------------
1101 GAAGCCAGAA AAACACCTGT AACTCAAACC CCAACTCAAG CAAGTAACTC CCAGTTCATC CCCATTCATC ACCCTGGAGC CTTCCCTCCT CTTCCCAGCA
     CTTCGGTCTT TTTGTGGACA TTGAGTTTGG GGTTGAGTTC GTTCATTGAG GGTCAAGTAG GGGTAAGTAG TGGGACCTCG GAAGGGAGGA GAAGGGTCGT

+3   ArgProGlyPhe ProProPro ThrTyrValIle ProProPro ValAlaPhe SerMetGlySer GlyTyrThr PheProAla GlyValSerVal ProGlyThr
     ----------------------------------------------------------------------------------------------------
1201 GGCCAGGGTT TCCGCCCCCA ACATATGTTA TCCCCCCGCC TGTGGCATTT TCTATGGGCT CAGGTTACAC CTTCCCAGCT GGTGTTTCTG TCCCAGGAAC
     CCGGTCCCAA AGGCGGGGGT TGTATACAAT AGGGGGGCGG ACACCGTAAA AGATACCCGA GTCCAATGTG GAAGGGTCGA CCACAAAGAC AGGGTCCTTG

+3   ThrPheLeuGln ProThrAlaHis SerProAla GlyAsnGln ValGlnAlaGly LysGlnSer HisIlePro TyrSerGlnGln ArgProSer GlyProGly
     ----------------------------------------------------------------------------------------------------
1301 CTTTCTTCAG CCTACAGCTC ACTCTCCAGC AGGAAACCAG GTGCAAGCTG GGAAACAGTC CCACATTCCT TACAGCCAGC AACGGCCCTC TGGACCAGGG
     GAAAGAAGTC GGATGTCGAG TGAGAGGTCG TCCTTTGGTC CACGTTCGAC CCTTTGTCAG GGTGTAAGGA ATGTCGGTCG TTGCCGGGAG ACCTGGTCCC

+3   ProMetAsnGln GlyProGln GlnSerGln ProProSerGln GlnProLeu ThrSerLeu ProAlaGlnPro ThrAlaGln SerThrSer GlnLeuGlnVal
     ----------------------------------------------------------------------------------------------------
1401 CCAATGAACC AGGGACCTCA ACAATCACAG CCACCTTCCC AGCAACCCCT TACATCTTTA CCAGCTCAGC CAACAGCACA GTCTACAAGC CAGCTGCAGG
     GGTTACTTGG TCCCTGGAGT TGTTAGTGTC GGTGGAAGGG TCGTTGGGGA ATGTAGAAAT GGTCGAGTCG GTTGTCGTGT CAGATGTTCG GTCGACGTCC
```

FIG. 1C

```
  +3  ValGlnAlaLeu ThrGlnGln GlnGlnSerPro ThrLysAla ValProAla LeuGlyLysSer ProProHis HisSerGly PheGlnGlnTyr GlnGlnAla
      ----------------------------------------------------------------------------------------------------------
1501  TTCAAGCTCT AACTCAGCAA CAACAATCCC CTACAAAAGC TGTGCCGGCT TTGGGGAAAA GCCCGCCTCA CCACTCTGGA TTCCAGCAGT ATCAACAGGC
      AAGTTCGAGA TTGAGTCGTT GTTGTTAGGG GATGTTTTCG ACACGGCCGA AACCCCTTTT CGGGCGGAGT GGTGAGACCT AAGGTCGTCA TAGTTGTCCG

  +3 AlaAspAlaSer LysGlnLeuTrp AsnProPro GlnValGln GlyProLeuGly LysIleMet ProValLys GlnProTyrTyr LeuGlnThr GlnAspPro
      ----------------------------------------------------------------------------------------------------------
1601  AGATGCCTCC AAACAGCTGT GGAATCCCCC TCAGGTTCAA GGTCCATTAG GGAAAATTAT GCCTGTGAAA CAGCCCTACT ACCTTCAGAC CCAAGACCCC
      TCTACGGAGG TTTGTCGACA CCTTAGGGGG AGTCCAAGTT CCAGGTAATC CCTTTTAATA CGGACACTTT GTCGGGATGA TGGAAGTCTG GGTTCTGGGG

  +3  IleLysLeuPhe GluProSer LeuGlnPro ProValMetGln GlnGlnPro LeuGluLys LysMetLysPro PheProMet GluProTyr AsnHisAsnPro
      ----------------------------------------------------------------------------------------------------------
1701  ATAAAACTGT TTGAGCCGTC ATTGCAACCT CCTGTAATGC AGCAGCAGCC TCTAGAAAAA AAAATGAAGC CTTTTCCCAT GGAGCCATAT AACCATAATC
      TATTTTGACA AACTCGGCAG TAACGTTGGA GGACATTACG TCGTCGTCGG AGATCTTTTT TTTTACTTCG GAAAAGGGTA CCTCGGTATA TTGGTATTAG

  +3  ProSerGluVal LysValPro GluPheTyrTrp AspSerSer TyrSerMet AlaAspAsnArg SerValMet AlaGlnGln AlaAsnIleAsp ArgArgGly
      ----------------------------------------------------------------------------------------------------------
1801  CCTCAGAAGT CAAGGTCCCA GAATTCTACT GGGATTCTTC CTACAGCATG GCTGATAACA GATCTGTAAT GGCACAGCAA GCAAACATAG ACCGCAGGGG
      GGAGTCTTCA GTTCCAGGGT CTTAAGATGA CCCTAAGAAG GATGTCGTAC CGACTATTGT CTAGACATTA CCGTGTCGTT CGTTTGTATC TGGCGTCCCC

  +3 GlyLysArgSer ProGlyValPhe ArgProGlu GlnAspPro ValProArgMet ProPheGlu LysSerLeu LeuGluLysPro SerGluLeu MetSerHis
      ----------------------------------------------------------------------------------------------------------
1901  CAAACGGTCA CCAGGAGTCT TCCGTCCAGA GCAGGATCCT GTACCCAGAA TGCCGTTTGA GAAATCCTTA TTGGAGAAGC CCTCAGAGCT CATGTCACAT
      GTTTGCCAGT GGTCCTCAGA AGGCAGGTCT CGTCCTAGGA CATGGGTCTT ACGGCAAACT CTTTAGGAAT AACCTCTTCG GGAGTCTCGA GTACAGTGTA

  +3  SerSerSerPhe LeuSerLeu ThrGlyPhe SerLeuAsnGln GluArgTyr ProAsnAsn SerMetPheAsn GluValTyr GlyLysAsn LeuThrSerSer
      ----------------------------------------------------------------------------------------------------------
2001  TCATCCTCTT TCCTGTCCCT CACCGGATTC TCTCTCAATC AGGAAAGATA CCCAAATAAT AGTATGTTCA ATGAGGTATA TGGGAAAAAC CTGACATCCA
      AGTAGGAGAA AGGACAGGGA GTGGCCTAAG AGAGAGTTAG TCCTTTCTAT GGGTTTATTA TCATACAAGT TACTCCATAT ACCCTTTTTG GACTGTAGGT

  +3  SerSerLysAla GluLeuSer ProSerMetAla ProGlnGlu ThrSerLeu TyrSerLeuPhe GluGlyThr ProTrpSer ProSerLeuPro AlaSerSer
      ----------------------------------------------------------------------------------------------------------
2101  GCTCCAAAGC AGAACTCAGT CCCTCAATGG CCCCCCAGGA AACATCTCTG TATTCCCTTT TTGAAGGGAC TCCGTGGTCT CCATCACTTC CTGCCAGTTC
      CGAGGTTTCG TCTTGAGTCA GGGAGTTACC GGGGGGTCCT TTGTAGAGAC ATAAGGGAAA AACTTCCCTG AGGCACCAGA GGTAGTGAAG GACGGTCAAG
```

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FIG. 1D

```
  +3 SerAspHisSer ThrProAlaSer GlnSerPro HisSerSer AsnProSerSer LeuProSer SerProPro ThrHisAsnHis AsnSerVal ProPheSer
     ---------------------------------------------------------------------------------------------------------
2201 AGATCATTCA ACACCAGCCA GCCAGTCTCC TCATTCCTCT AACCCAAGCA GCCTACCCAG CTCTCCTCCA ACACACAACC ATAATTCTGT TCCATTCTCC
     TCTAGTAAGT TGTGGTCGGT CGGTCAGAGG AGTAAGGAGA TTGGGTTCGT CGGATGGGTC GAGAGGAGGT TGTGTGTTGG TATTAAGACA AGGTAAGAGG

  +3 AsnPheGlyPro IleGlyThr ProAspAsn ArgAspArgArg ThrAlaAsp ArgTrpLys ThrAspLysPro AlaMetGly GlyPheGly IleAspTyrLeu
     ---------------------------------------------------------------------------------------------------------
2301 AATTTTGGAC CCATTGGGAC TCCAGATAAC AGGGATAGAA GGACTGCAGA TCGGTGGAAA ACTGATAAGC CAGCCATGGG TGGGTTTGGC ATTGATTATC
     TTAAAACCTG GGTAACCCTG AGGTCTATTG TCCCTATCTT CCTGACGTCT AGCCACCTTT TGACTATTCG GTCGGTACCC ACCCAAACCG TAACTAATAG

  +3 LeuSerAlaThr SerSerSer GluSerSerTrp HisGlnAla SerThrPro SerGlyThrTrp ThrGlyHis GlyProSer MetGluAspSer SerAlaVal
     ---------------------------------------------------------------------------------------------------------
2401 TCTCAGCAAC GTCATCCTCT GAGAGCAGTT GGCATCAGGC CAGCACTCCG AGTGGCACCT GGACAGGCCA TGGCCCTTCC ATGGAGGATT CCTCTGCTGT
     AGAGTCGTTG CAGTAGGAGA CTCTCGTCAA CCGTAGTCCG GTCGTGAGGC TCACCGTGGA CCTGTCCGGT ACCGGGAAGG TACCTCCTAA GGAGACGACA

  +3 ValLeuMetGlu SerLeuLysSer IleTrpSer SerSerMet MetHisProGly ProSerAla LeuGluGln LeuLeuMetGln GlnLysGln LysGlnGln
     ---------------------------------------------------------------------------------------------------------
2501 CCTCATGGAA AGCCTAAAGT CTATCTGGTC CAGTTCCATG ATGCATCCTG GACCTTCTGC TCTGGAGCAG CTGTTAATGC AGCAGAAGCA GAAACAGCAA
     GGAGTACCTT TCGGATTTCA GATAGACCAG GTCAAGGTAC TACGTAGGAC CTGGAAGACG AGACCTCGTC GACAATTACG TCGTCTTCGT CTTTGTCGTT

  +3 ArgGlyGlnGly ThrMetAsn ProProHis ***
     ----------------------------------
2601 CGGGGACAAG GCACCATGAA CCCTCCACAC TGAGGCCAAA GTGGCAACCT GGGAATGAAG GCTCCATAAA CCATGGCATG TTGGGTTTGC AGGACTGGCC
     GCCCCTGTTC CGTGGTACTT GGGAGGTGTG ACTCCGGTTT CACCGTTGGA CCCTTACTTC CGAGGTATTT GGTACCGTAC AACCCAAACG TCCTGACCGG
2701 CACACAGTCC CCTGCAGGTG GCAGCCCTCT TTTCTGTTTC TCGCTGTCAA GAGGGTGTAA GTATTCCACC AGCCCGCTGA GTGTGCACGA AATGTTCGCA
     GTGTGTCAGG GGACGTCCAC CGTCGGGAGA AAAGACAAAG AGCGACAGTT CTCCCACATT CATAAGGTGG TCGGGCGACT CACACGTGCT TTACAAGCGT
2801 GTGCAACAAA AAGAAAAATC CATCAGGAAC TCTCCGTCCC CCCGGGGCCT TCCGGAGGGA GAGAGAGAGG AACTGCTGTT TATCTCACTC AGTTACTTGG
     CACGTTGTTT TTCTTTTTAG GTAGTCCTTG AGAGGCAGGG GGGCCCCGGA AGGCCTCCCT CTCTCTCTCC TTGACGACAA ATAGAGTGAG TCAATGAACC
2901 TATCACCGCC TCTCACC
     ATAGTGGCGG AGAGTGG
```

FIG. 2A

```
  1  ACCTGAGTAA GAGCTTGGAA AAGTTGAGCC CTCTTCGAGA GAAATTGGAA GAACAGTTTA AGAGGCTGCT ATTCCAAAAA GCTTTCAACT CTCAGCAGTT
     TGGACTCATT CTCGAACCTT TTCAACTCGG GAGAAGCTCT CTTTAACCTT CTTGTCAAAT TCTCCGACGA TAAGGTTTTT CGAAAGTTGA GAGTCGTCAA
101  AGTTCATGTC ATTGTCATTA ACCTGTTTCA ACTTCATCAC CTTCGTGACT TTAGCAATGA AACCGAGCAG CACACTTATA GCCAAGATGA GCAGCTATGT
     TCAAGTACAG TAACAGTAAT TGGACAAAGT TGAAGTAGTG GAAGCACTGA AATCGTTACT TTGGCTCGTC GTGTGAATAT CGGTTCTACT CGTCGATACA

 +3                                MetSer PheLeuGlyIle LeuCysLys CysProLeu GlnAsnGluSer GlnGluGlu SerTyrAsn AlaTyrProLeu
                                   --------------------------------------------------------------------------------
201  TGGACACAGT TGCTGGCCCT CTTTATGTCT TTTCTTGGCA TCCTGTGCAA GTGTCCTCTA CAGAATGAGT CTCAGGAGGA GTCCTACAAT GCCTATCCTC
     ACCTGTGTCA ACGACCGGGA GAAATACAGA AAAGAACCGT AGGACACGTT CACAGGAGAT GTCTTACTCA GAGTCCTCCT CAGGATGTTA CGGATAGGAG

 +3  LeuProAlaVal LysValSer MetAspTrpLeu ArgLeuArg ProArgVal PheGlnGluAla ValValAsp GluArgGln TyrIleTrpPro TrpLeuIle
     ------------------------------------------------------------------------------------------------------------
301  TTCCAGCAGT CAAGGTCTCC ATGGACTGGC TAAGACTCAG ACCCAGGGTC TTTCAGGAGG CAGTGGTGGA TGAAAGACAG TACATTTGGC CCTGGTTGAT
     AAGGTCGTCA GTTCCAGAGG TACCTGACCG ATTCTGAGTC TGGGTCCCAG AAAGTCCTCC GTCACCACCT ACTTTCTGTC ATGTAAACCG GGACCAACTA

 +3 IleSerLeuLeu AsnSerPheHis ProHisGlu GluAspLeu SerSerIleSer AlaThrPro LeuProGlu GluPheGluLeu GlnGlyPhe LeuAlaLeu
     ------------------------------------------------------------------------------------------------------------
401  TTCTCTTCTG AATAGTTTCC ATCCCCATGA AGAGGACCTC TCAAGTATTA GTGCGACACC ACTTCCAGAG GAGTTTGAAT TACAAGGATT TTTGGCATTG
     AAGAGAAGAC TTATCAAAGG TAGGGGTACT TCTCCTGGAG AGTTCATAAT CACGCTGTGG TGAAGGTCTC CTCAAACTTA ATGTTCCTAA AAACCGTAAC

 +3  ArgProSerPhe ArgAsnLeu AspPheSer LysGlyHisGln GlyIleThr GlyAspLys GluGlyGlnGln ArgArgIle ArgGlnGln ArgLeuIleSer
     ------------------------------------------------------------------------------------------------------------
501  AGACCTTCTT TCAGGAACTT GGATTTTTCC AAAGGTCACC AGGGTATTAC AGGGGACAAA GAAGGCCAGC AACGACGAAT ACGACAGCAA CGCTTGATCT
     TCTGGAAGAA AGTCCTTGAA CCTAAAAAGG TTTCCAGTGG TCCCATAATG TCCCCTGTTT CTTCCGGTCG TTGCTGCTTA TGCTGTCGTT GCGAACTAGA

 +3  SerIleGlyLys TrpIleAla AspAsnGlnPro ArgLeuIle GlnCysGlu AsnGluValGly LysLeuLeu PheIleThr GluIleProGlu LeuIleLeu
     ------------------------------------------------------------------------------------------------------------
601  CTATAGGCAA ATGGATTGCT GATAATCAGC CAAGGCTGAT TCAGTGTGAA AATGAGGTAG GGAAATTGTT GTTTATCACA GAAATCCCAG AATTAATACT
     GATATCCGTT TACCTAACGA CTATTAGTCG GTTCCGACTA AGTCACACTT TTACTCCATC CCTTTAACAA CAAATAGTGT CTTTAGGGTC TTAATTATGA

 +3 LeuGluAspPro SerGluAlaLys GluAsnLeu IleLeuGln GluThrSerVal IleGluSer LeuAlaAla AspGlySerPro GlyLeuLys SerValLeu
     ------------------------------------------------------------------------------------------------------------
701  GGAAGACCCC AGTGAAGCCA AAGAGAACCT CATTCTGCAA GAAACATCTG TGATAGAGTC GTTGGCTGCA GATGGGAGCC CAGGGCTAAA ATCAGTGCTA
     CCTTCTGGGG TCACTTCGGT TTCTCTTGGA GTAAGACGTT CTTTGTAGAC ACTATCTCAG
     CAACCGACGT CTACCCTCGG GTCCCGATTT TAGTCACGAT
```

FIG. 2B

```
  +3  SerThrSerArg AsnLeuSer AsnAsnCys AspThrGlyGlu LysProVal ValThrPhe LysGluAsnIle LysThrArg GluValAsn ArgAspGlnGly
      -----------------------------------------------------------------------------------------------------------
 801  TCTACAAGCC GAAATTTAAG CAACAACTGC GACACAGGAG AGAAGCCAGT GGTTACCTTC AAAGAAAACA TTAAGACACG AGAAGTGAAC AGAGACCAAG
      AGATGTTCGG CTTTAAATTC GTTGTTGACG CTGTGTCCTC TCTTCGGTCA CCAATGGAAG TTTCTTTTGT AATTCTGTGC TCTTCACTTG TCTCTGGTTC

  +3 GlyArgSerPhe ProProLys GluValLysSer GlnThrGly LeuArgLys ThrProValSer GluAlaArg LysThrPro ValThrGlnThr ProThrGln
      -----------------------------------------------------------------------------------------------------------
 901  GAAGAAGTTT TCCTCCCAAA GAGGTAAAAT CCCAGACAGG ACTAAGAAAG ACTCCAGTGT CTGAAGCCAG AAAAACACCT GTAACTCAAA CCCCAACTCA
      CTTCTTCAAA AGGAGGGTTT CTCCATTTTA GGGTCTGTCC TGATTCTTTC TGAGGTCACA GACTTCGGTC TTTTTGTGGA CATTGAGTTT GGGGTTGAGT

  +3 GlnAlaSerAsn SerGlnPheIle ProIleHis HisProGly AlaPheProPro LeuProSer ArgProGly PheProProPro ThrTyrVal IleProPro
      -----------------------------------------------------------------------------------------------------------
1001  AGCAAGTAAC TCCCAGTTCA TCCCCATTCA TCACCCTGGA GCCTTCCCTC CTCTTCCCAG CAGGCCAGGG TTTCCGCCCC CAACATATGT TATCCCCCCG
      TCGTTCATTG AGGGTCAAGT AGGGGTAAGT AGTGGGACCT CGGAAGGGAG GAGAAGGGTC GTCCGGTCCC AAAGGCGGGG GTTGTATACA ATAGGGGGGC

  +3  ProValAlaPhe SerMetGly SerGlyTyr ThrPheProAla GlyValSer ValProGly ThrPheLeuGln ProThrAla HisSerPro AlaGlyAsnGln
      -----------------------------------------------------------------------------------------------------------
1101  CCTGTGGCAT TTTCTATGGG CTCAGGTTAC ACCTTCCCAG CTGGTGTTTC TGTCCCAGGA ACCTTTCTTC AGCCTACAGC TCACTCTCCA GCAGGAAACC
      GGACACCGTA AAAGATACCC GAGTCCAATG TGGAAGGGTC GACCACAAAG ACAGGGTCCT TGGAAAGAAG TCGGATGTCG AGTGAGAGGT CGTCCTTTGG

  +3 GlnValGlnAla GlyLysGln SerHisIlePro TyrSerGln GlnArgPro SerGlyProGly ProMetAsn GlnGlyPro GlnGlnSerGln ProProSer
      -----------------------------------------------------------------------------------------------------------
1201  AGGTGCAAGC TGGGAAACAG TCCCACATTC CTTACAGCCA GCAACGGCCC TCTGGACCAG GGCCAATGAA CCAGGGACCT CAACAATCAC AGCCACCTTC
      TCCACGTTCG ACCCTTTGTC AGGGTGTAAG GAATGTCGGT CGTTGCCGGG AGACCTGGTC CCGGTTACTT GGTCCCTGGA GTTGTTAGTG TCGGTGGAAG

  +3 SerGlnGlnPro LeuThrSerLeu ProAlaGln ProThrAla GlnSerThrSer GlnLeuGln ValGlnAla LeuThrGlnGln GlnGlnSer ProThrLys
      -----------------------------------------------------------------------------------------------------------
1301  CCAGCAACCC CTTACATCTT TACCAGCTCA GCCAACAGCA CAGTCTACAA GCCAGCTGCA GGTTCAAGCT CTAACTCAGC AACAACAATC CCCTACAAAA
      GGTCGTTGGG GAATGTAGAA ATGGTCGAGT CGGTTGTCGT GTCAGATGTT CGGTCGACGT CCAAGTTCGA GATTGAGTCG TTGTTGTTAG GGGATGTTTT

  +3  AlaValProAla LeuGlyLys SerProPro HisHisSerGly PheGlnGln TyrGlnGln AlaAspAlaSer LysGlnLeu TrpAsnPro ProGlnValGln
      -----------------------------------------------------------------------------------------------------------
1401  GCTGTGCCGG CTTTGGGGAA AAGCCCGCCT CACCACTCTG GATTCCAGCA GTATCAACAG GCAGATGCCT CCAAACAGCT GTGGAATCCC CCTCAGGTTC
      CGACACGGCC GAAACCCCTT TTCGGGCGGA GTGGTGAGAC CTAAGGTCGT CATAGTTGTC CGTCTACGGA GGTTTGTCGA CACCTTAGGG GGAGTCCAAG
```

FIG. 2C

```
  +3  GlnGlyProLeu GlyLysIle MetProValLys GlnProTyr TyrLeuGln ThrGlnAspPro IleLysLeu PheGluPro SerLeuGlnPro ProValMet
      ----------------------------------------------------------------------------------------------------------------
1501  AAGGCCCATT AGGGAAAATT ATGCCTGTGA AACAGCCCTA CTACCTTCAG ACCCAAGACC CCATAAAACT GTTTGAGCCG TCATTGCAAC CTCCTGTAAT
      TTCCGGGTAA TCCCTTTTAA TACGGACACT TTGTCGGGAT GATGGAAGTC TGGGTTCTGG GGTATTTTGA CAAACTCGGC AGTAACGTTG GAGGACATTA

  +3 MetGlnGlnGln ProLeuGluLys LysMetLys ProPhePro MetGluProTyr AsnHisAsn ProSerGlu ValLysValPro GluPheTyr TrpAspSer
      ----------------------------------------------------------------------------------------------------------------
1601  GCAGCAGCAG CCTCTAGAAA AAAAAATGAA GCCTTTTCCC ATGGAGCCAT ATAACCATAA TCCCTCAGAA GTCAAGGTCC CAGAATTCTA CTGGGATTCT
      CGTCGTCGTC GGAGATCTTT TTTTTTACTT CGGAAAAGGG TACCTCGGTA TATTGGTATT AGGGAGTCTT CAGTTCCAGG GTCTTAAGAT GACCCTAAGA

  +3  SerTyrSerMet AlaAspAsn ArgSerVal MetAlaGlnGln AlaAsnIle AspArgArg GlyLysArgSer ProGlyVal PheArgPro GluGlnAspPro
      ----------------------------------------------------------------------------------------------------------------
1701  TCCTACAGCA TGGCTGATAA CAGATCTGTA ATGGCACAAC AAGCAAACAT AGACCGCAGG GGCAAACGGT CACCAGGAGT CTTCCGTCCA GAGCAGGATC
      AGGATGTCGT ACCGACTATT GTCTAGACAT TACCGTGTTG TTCGTTTGTA TCTGGCGTCC CCGTTTGCCA GTGGTCCTCA GAAGGCAGGT CTCGTCCTAG

  +3  ProValProArg MetProPhe GluLysSerLeu LeuGluLys ProSerGlu LeuMetSerHis SerSerSer PheLeuSer LeuThrGlyPhe SerLeuAsn
      ----------------------------------------------------------------------------------------------------------------
1801  CTGTACCCAG AATGCCGTTT GAGAAATCCT TATTGGAGAA GCCCTCAGAG CTCATGTCAC ATTCATCCTC TTTCCTGTCC CTCACCGGAT TCTCTCTCAA
      GACATGGGTC TTACGGCAAA CTCTTTAGGA ATAACCTCTT CGGGAGTCTC GAGTACAGTG TAAGTAGGAG AAAGGACAGG GAGTGGCCTA AGAGAGAGTT

  +3 AsnGlnGluArg TyrProAsnAsn SerMetPhe AsnGluVal TyrGlyLysAsn LeuThrSer SerSerLys AlaGluLeuSer ProSerMet AlaProGln
      ----------------------------------------------------------------------------------------------------------------
1901  TCAGGAAAGA TACCCAAATA ATAGTATGTT CAATGAGGTA TATGGGAAAA ACCTGACATC CAGCTCCAAA GCAGAACTCA GTCCCTCAAT GGCCCCCCAG
      AGTCCTTTCT ATGGGTTTAT TATCATACAA GTTACTCCAT ATACCCTTTT TGGACTGTAG GTCGAGGTTT CGTCTTGAGT CAGGGAGTTA CCGGGGGGTC

  +3  GluThrSerLeu TyrSerLeu PheGluGly ThrProTrpSer ProSerLeu ProAlaSer SerAspHisSer ThrProAla SerGlnSer ProHisSerSer
      ----------------------------------------------------------------------------------------------------------------
2001  GAAACATCTC TGTATTCCCT TTTTGAAGGG ACTCCGTGGT CTCCATCACT TCCTGCCAGT TCAGATCATT CAACACCAGC CAGCCAGTCT CCTCATTCCT
      CTTTGTAGAG ACATAAGGGA AAAACTTCCC TGAGGCACCA GAGGTAGTGA AGGACGGTCA AGTCTAGTAA GTTGTGGTCG GTCGGTCAGA GGAGTAAGGA

  +3  SerAsnProSer SerLeuPro SerSerProPro ThrHisAsn HisAsnSer ValProPheSer AsnPheGly ProIleGly ThrProAspAsn ArgAspArg
      ----------------------------------------------------------------------------------------------------------------
2101  CTAACCCAAG CAGCCTACCC AGCTCTCCTC CAACACACAA CCATAATTCT GTTCCATTCT CCAATTTTGG ACCCATTGGG ACTCCAGATA ACAGGGATAG
      GATTGGGTTC GTCGGATGGG TCGAGAGGAG GTTGTGTGTT GGTATTAAGA CAAGGTAAGA GGTTAAAACC TGGGTAACCC TGAGGTCTAT TGTCCCTATC
```

FIG. 2D

```
  +3 ArgArgThrAla AspArgTrpLys ThrAspLys ProAlaMet GlyGlyPheGly IleAspTyr LeuSerAla ThrSerSerSer GluSerSer TrpHisGln
     ----------------------------------------------------------------------------------------------------------
2201 AAGGACTGCA GATCGGTGGA AAACTGATAA GCCAGCCATG GGTGGGTTTG GCATTGATTA TCTCTCAGCA ACGTCATCCT CTGAGAGCAG TTGGCATCAG
     TTCCTGACGT CTAGCCACCT TTTGACTATT CGGTCGGTAC CCACCCAAAC CGTAACTAAT AGAGAGTCGT TGCAGTAGGA GACTCTCGTC AACCGTAGTC

  +3 AlaSerThrPro SerGlyThr TrpThrGly HisGlyProSer MetGluAsp SerSerAla ValLeuMetGlu SerLeuLys SerIleTrp SerSerSerMet
     ----------------------------------------------------------------------------------------------------------
2301 GCCAGCACTC CGAGTGGCAC CTGGACAGGC CATGGCCCTT CCATGGAGGA TTCCTCTGCT GTCCTCATGG AAAGCCTAAA GTCTATCTGG TCCAGTTCCA
     CGGTCGTGAG GCTCACCGTG GACCTGTCCG GTACCGGGAA GGTACCTCCT AAGGAGACGA CAGGAGTACC TTTCGGATTT CAGATAGACC AGGTCAAGGT

  +3 MetMetHisPro GlyProSer AlaLeuGluGln LeuLeuMet GlnGlnLys GlnLysGlnGln ArgGlyGln GlyThrMet AsnProProHis ***
     -----------------------------------------------------------------------------------------------------
2401 TGATGCATCC TGGACCTTCT GCTCTGGAGC AGCTGTTAAT GCAGCAGAAG CAGAAACAGC AACGGGGACA AGGCACCATG AACCCTCCAC ACTGAGGCCA
     ACTACGTAGG ACCTGGAAGA CGAGACCTCG TCGACAATTA CGTCGTCTTC GTCTTTGTCG TTGCCCCTGT TCCGTGGTAC TTGGGAGGTG TGACTCCGGT
2501 AAGTGGCAAC CTGGGAATGA AGGCTCCATA AACCATGGCA TGTTGGGTTT GCAGGACTGG CCCACACAGT CCCCTGCAGG TGGCAGCCCT CTTTTCTGTT
     TTCACCGTTG GACCCTTACT TCCGAGGTAT TTGGTACCGT ACAACCCAAA CGTCCTGACC GGGTGTGTCA GGGGACGTCC ACCGTCGGGA GAAAAGACAA
2601 TCTCGCTGTC AAGAGGGTGT AAGTATTCCA CCAGCCCGCT GAGTGTGCAC GAAATGTTCG CAGTGCAACA AAAAGAAAAA TCCATCAGGA ACTCTCCGTC
     AGAGCGACAG TTCTCCCACA TTCATAAGGT GGTCGGGCGA CTCACACGTG CTTTACAAGC GTCACGTTGT TTTTCTTTTT AGGTAGTCCT TGAGAGGCAG
2701 CCCCCGGGGC CTTCCGGAGG GAGAGAGAGA GGAACTGCTG TTTATCTCAC TCAGTTACTT GGTATCACCG CCTCTCACC
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FIG. 3

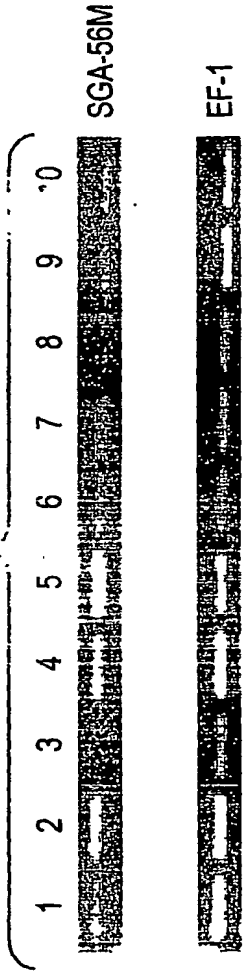


FIG. 4

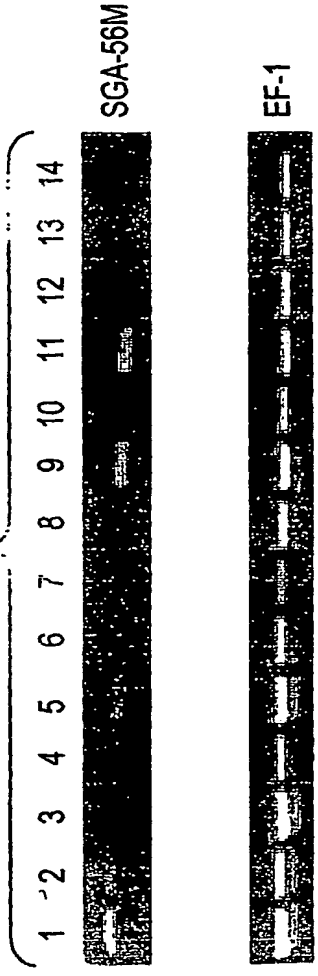


FIG. 5A

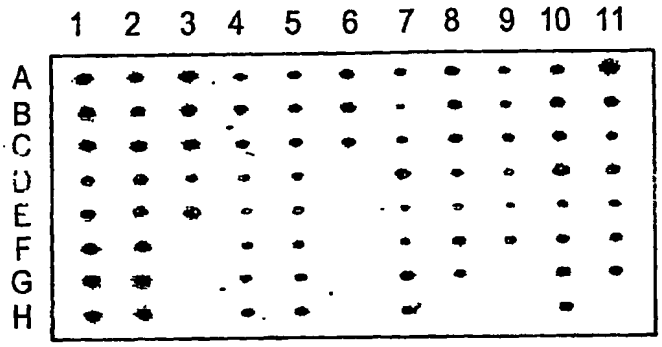


FIG. 5B

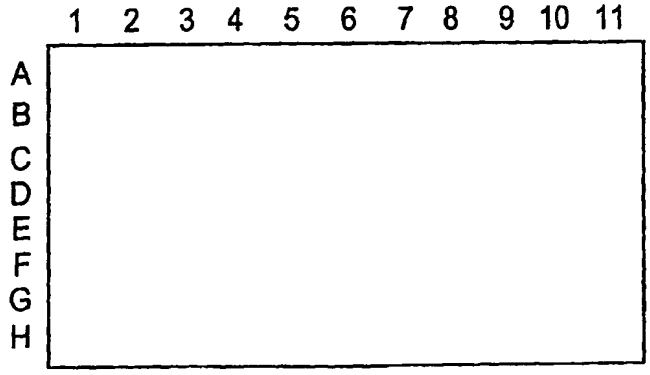


FIG. 6

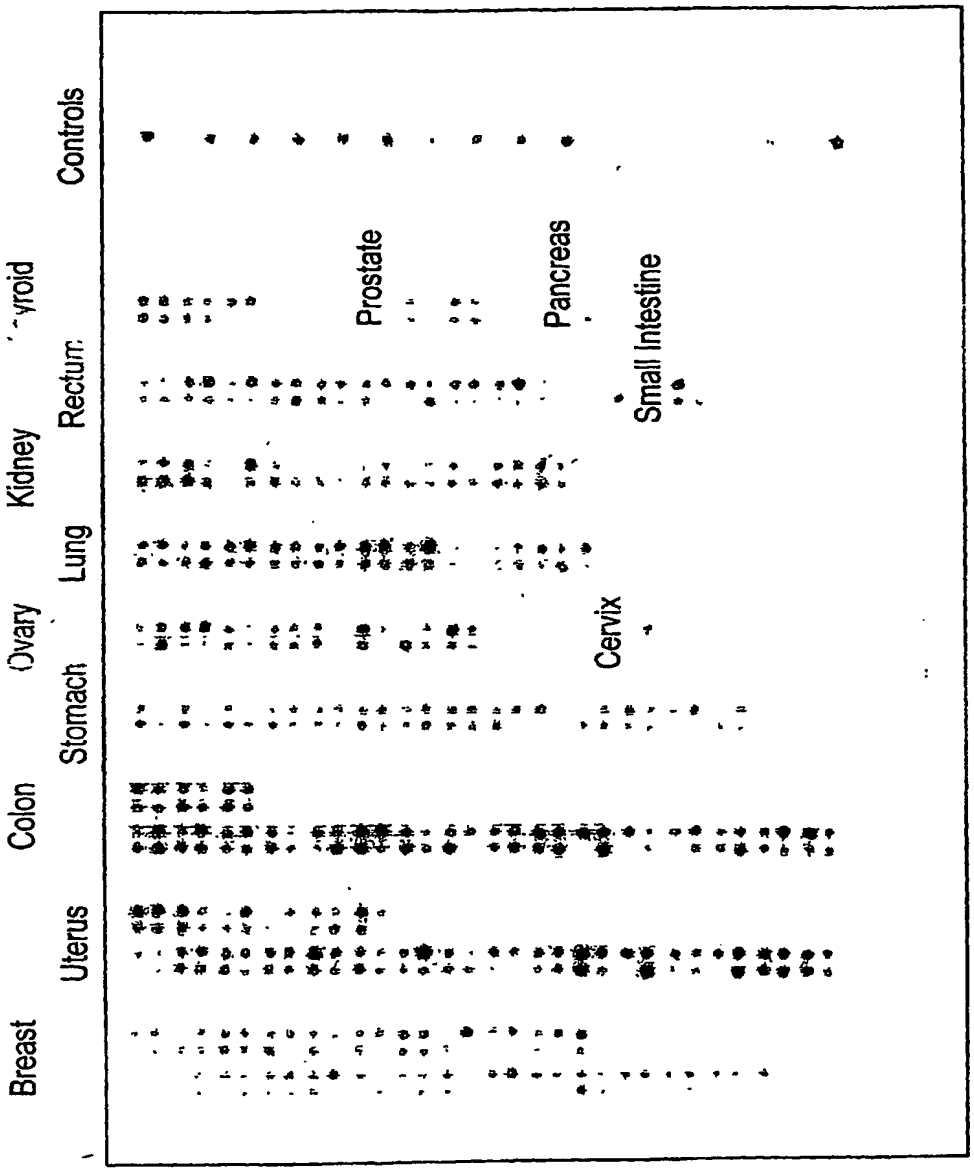

Breast
Uterus
Colon
Stomach
Ovary
Lung
Kidney
Rectum
Prostate
Pancreas
Cervix
Small Intestine
Controls

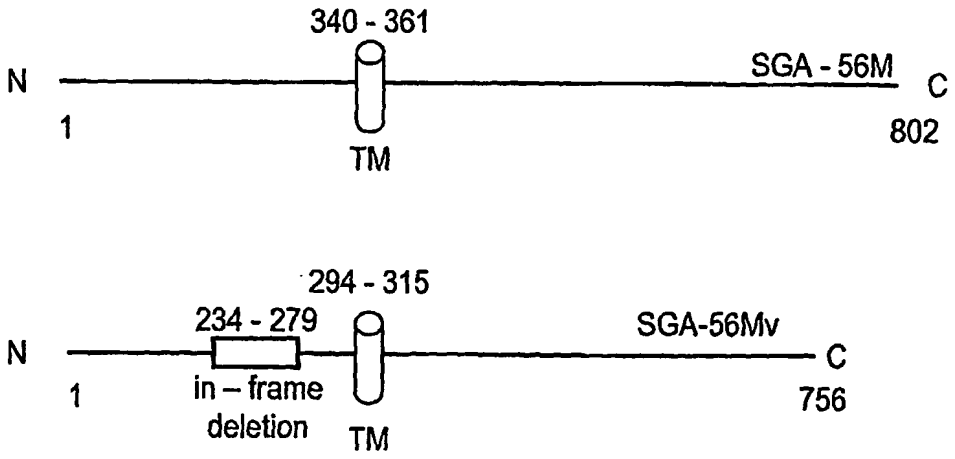
FIG. 7

```
  1  MSFLGILCKC PLQNESQEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
 51  RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
101  FSKGHQGITG DKEGQQRRIR QQRLISIGKW IADNQPRLIQ CENEVGKLLF
151  ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
201  NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVRRDYSK GITVTKNDGK
251  KDNNKRKTET KKCTLEKLQE TGKQNVAVQV KSQTELRKTP VSEARKTPVT
301  QTPTQASNSQ FIPIHHPGAF PPLPSRPGFP PPTYVIPPPV AFSMGSGYTF
351  PAGVSVPGTF LQPTAHSPAG NQVQAGKQSH IPYSQQRPSG PGPMNQGPQQ
401  SQPPSQQPLT SLPAQPTAQS TSQLQVQALT QQQQSPTKAV PALGKSPPHH
451  SGFQQYQQAD ASKQLWNPPQ VQGPLGKIMP VKQPYYLQTQ DPIKLFEPSL
501  QPPVMQQQPL EKKMKPFPME PYNHNPSEVK VPEFYWDSSY SMADNRSVMA
551  QQANIDRRGK RSPGVFRPEQ DPVPRMPFEK SLLEKPSELM SHSSSFLSLT
601  GFSLNQERYP NNSMFNEVYG KNLTSSSKAE LSPSMAPQET SLYSLFEGTP
651  WSPSLPASSD HSTPASQSPH SSNPSSLPSS PPTHNHNSVP FSNFGPIGTP
701  DNRDRRTADR WKTDKPAMGG FGIDYLSATS SSESSWHQAS TPSGTWTGHG
751  PSMEDSSAVL MESLKSIWSS SMMHPGPSAL EQLLMQQKQK QQRGQGTMNP
801  PH
```

FIG. 8

```
  1  MSFLGILCKC PLQNESQEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
 51  RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
101  FSKGHQGITG DKEGQQRRIR QQRLISIGKW IADNQPRLIQ CENEVGKLLF
151  ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
201  NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVKSQTGL RKTPVSEARK
251  TPVTQTPTQA SNSQFIPIHH PGAFPPLPSR PGFPPPTYVI PPPVAFSMGS
301  GYTFPAGVSV PGTFLQPTAH SPAGNQVQAG KQSHIPYSQQ RPSGPGPMNQ
351  GPQQSQPPSQ QPLTSLPAQP TAQSTSQLQV QALTQQQQSP TKAVPALGKS
401  PPHHSGFQQY QQADASKQLW NPPQVQGPLG KIMPVKQPYY LQTQDPIKLF
451  EPSLQPPVMQ QQPLEKKMKP FPMEPYNHNP SEVKVPEFYW DSSYSMADNR
501  SVMAQQANID RRGKRSPGVF RPEQDPVPRM PFEKSLLEKP SELMSHSSSF
551  LSLTGFSLNQ ERYPNNSMFN EVYGKNLTSS SKAELSPSMA PQETSLYSLF
601  EGTPWSPSLP ASSDHSTPAS QSPHSSNPSS LPSSPPTHNH NSVPFSNFGP
651  IGTPDNRDRR TADRWKTDKP AMGGFGIDYL SATSSSESSW HQASTPSGTW
701  TGHGPSMEDS SAVLMESLKS IWSSSMMHPG PSALEQLLMQ QKQKQQRGQG
751  TMNPPH
```

FIG. 9


340 - 361
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SGA - 56M
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TM
294 - 315
234 - 279
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